

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Horwath, K. L. et al.
- (ii) TITLE OF INVENTION: Nucleic Acids Sequences Encoding Type III Tenebrio Antifreeze Proteins and Method for Assaying Activity.
- (iii) NUMBER OF SEQUENCES: 48
- (iv) CORRESPONDENCE ADDRESS
 - (A) ADDRESSEE: Dr. Kathleen L. Horwath
 - (B) STREET: Department of Biological Sciences, Binghamton University
 - (C) CITY: Binghamton
 - (D) STATE: New York
 - (E) ZIP: 13902-6000
- (v) COMPUTER READABLE FORM
 - (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
 - (B) COMPUTER: IBM AT/ATX compatible
 - (C) OPERATING SYSTEM: Windows 95/98
 - (D) SOFTWARE: Microsoft Word
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA
 - (A) APPLICATION NUMBER: 60210446
 - (B) FILING DATE: June 8, 2000
- (viii) ATTORNEY/AGENT INFORMATION
 - (A) NAME: Mark Levy, Attorney-at-Law
 - (B) REGISTRATION NUMBER: 29,188
 - (C) REFERENCE/DOCKET NUMBER: RB125
- (ix) TELECOMMUNICATION INFORMATION
 - (A) TELEPHONE: 607-722-6600
 - (B) TELEFAX: 607-724-2207

09876543210

Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val
1 5 10 15

(A) ORGANISM: *Tenebrio molitor*
(B) INDIVIDUAL/ISOLATE: none
(C) CELL TYPE: fat body and whole organism

(ii) MOLECULE TYPE: Peptide

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v) FRAGMENT TYPE: N-terminal fragment

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY:

(B) CLONE:

(ix) FEATURES:

(D) OTHER INFORMATION: N-terminal sequence of protein Tm 12.8b

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val
1 5 10 15

(2) INFORMATION FOR SEQ. ID NO: 2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 566 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 13.17

(ix) FEATURES

- (D) OTHER INFORMATION: Non-his-tagged, signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GTGGATCCAA AGAATTCGGC ACGAGACTAC TAAG ATG AAG TTG CTC	36
Met Lys Leu Leu	
-15	
TGT TGT CTA ATC TCC CTC ATT CTG TTG GTC ACA GTT CAG GCC CTG	81
Cys Cys Leu Ile Ser Leu Ile Leu Leu Val Thr Val Gln Ala Leu	
-10 -5 1	
ACC GAG GCA CAA ATT GAG AAA CTG AAC AAG ATC AGC AAA AAA TGT	126
Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys	
5 10 15	
CAA AAT GAA AGT GGA GTG TCG CAA GAG ATC ATA ACC AAA GCT CGC	171
Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala Arg	
20 25 30	
AAC GGT GAC TGG GAG GAC GAT CCT AAA CTG AAA CGC CAA GTT TTT	216
Asn Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe	
35 40 45	
TGC GTG GCC AGG AAC GCC GGT CTG GCC ACG GAA TCG GGA GAG GTG	261
Cys Val Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val	
50 55 60	
GTG GTC GAC GTG TTG AGG GAG AAG GTG AGG AAG GTC ACT GAC AAC	306
Val Val Asp Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn	
65 70 75	
GAC GAA GAA ACT GAG AAA ATC ATC AAT AAG TGC GCC GTC AAG AGA	351
Asp Glu Glu Thr Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg	
80 85 90	
GAT ACT GTT GAA GAG ACG GTG TTC AAT ACT TTC AAA TGT GTC ATG	396
Asp Thr Val Glu Glu Thr Val Phe Asn Thr Phe Lys Cys Val Met	
95 100 105	
AAA AAC AAG CCA AAG TTC TCA CCA GTT GAT TGA ACCACCACGA	439
Lys Asn Lys Pro Lys Phe Ser Pro Val Asp *	
110 115	
CTAGTAGATG GTTCAAATGG TGTGCTTTAC ATATAAAAAT AAAGTGTTTC	489
TGATGTAAAA AAAAAAAAAA AAAAAAAAAA AACTCGAGAG TATTCTAGAG	539
CGGCCGCGGG CCCATCGTTT TCCACCC	566

(2) INFORMATION FOR SEQ. ID NO: 3

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 13.17

(ix) FEATURES

- (D) OTHER INFORMATION: Precursor Protein for Tm 13.17

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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Met Lys Leu Leu Cys Cys Leu Ile Ser Leu Ile Leu Leu Val Thr Val
  -15                      -10                      -5

Gln Ala Leu Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys
   1                      5                      10

Lys Cys Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala
 15                      20                      25                      30

Arg Asn Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe
 35                      40                      45

Cys Val Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val
 50                      55                      60

Val Asp Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu
 65                      70                      75

Glu Thr Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val
 80                      85                      90

Glu Glu Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro
 95                      100                      105                      110

Lys Phe Ser Pro Val Asp *
                  115

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09676756-060701

(2) INFORMATION FOR SEQ. ID NO: 4

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 13.17

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(ix)FEATURES
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(D) OTHER INFORMATION: Mature Protein for Tm 13.17

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
```

Leu Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys
1 5 10 15

Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn
20 25 30

Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys Val
35 40 45

Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp
50 55 60

Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr
65 70 75 80

Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu
85 90 95

Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys Phe
100 105 110

Ser Pro Val Asp *
115

(2) INFORMATION FOR SEQ. ID NO: 5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.2

(ix) FEATURES

- (D) OTHER INFORMATION: Non-His-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC	46
Met Lys Leu Leu Cys Phe Ala Phe Ala Ala	
-15 -10	
ATC GTC ATC GGA GCT CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA	91
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys	
-5 1 5	
AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC	136
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser	
10 15 20	
CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT	181
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp	
25 30 35	
CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA	226
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly	
40 45 50	
GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC	271
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala	
55 60 65	
AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG	316
Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val	
70 75 80	
CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT	361
Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr	
85 90 95	
GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT	406
Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro	
100 105 110	
ATT GAT TAA TTGTTTTGTA TTTGACTGAA TTTTGACAAT AAAGGTAATA	455
Ile Asp *	
115	
TCGTTATGTA AAAAAAAAAA AAAAAA	481

(2) INFORMATION FOR SEQ. ID NO: 7

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.2, 2.3, and 7.5

(ix) FEATURES

- (D) OTHER INFORMATION: Precursor Protein for Tm 12.84

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala
 -15 -10 -5

Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
 1 5 10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
 15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
 35 40 45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
 50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
 65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
 80 85 90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp
 95 100 105 110

Phe Ser Pro Ile Asp *
 115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Pro Ile Asp *

(2) INFORMATION FOR SEQ. ID NO: 9
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 481 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA to mRNA
 (iii) HYPOTHETICAL: no
 (iv) ANTI-SENSE: no
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Tenebrio molitor*
 (B) INDIVIDUAL/ISOLATE: none
 (C) CELL TYPE: fat body and whole organism
 (vii) IMMEDIATE SOURCE:
 (A) LIBRARY: cDNA
 (B) CLONE: 3.4
 (ix) FEATURES
 (D) OTHER INFORMATION: Non-His-tagged, Signal plus
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC	46
Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala	
-15 -10	
ATC GTC ATC GGA GCT CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA	91
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys	
-5 1 5	
AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC	136
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser	
10 15 20	
CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT	181
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp	
25 30 35	
CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA	226
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly	
40 45 50	
GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC	271
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala	
55 60 65	
AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG	316
Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val	
70 75 80	
CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT	361
Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr	
85 90 95	
GAC ACC TTC AAG GTT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT	406
Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro	
100 105 110	
ATT GAT TAA TTGTTTTGTA TTTGACTGAA TTTTGACAAT AAAGGTACTA	455
Ile Asp *	
115	
TCGTTATGTA AAAAAAAAAA AAAAAA	481

(2) INFORMATION FOR SEQ. ID NO: 10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 3.4

(ix) FEATURES

- (D) OTHER INFORMATION: Precursor Protein for Clone 3.4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

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Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala
  -15                      -10                      -5

Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
    1                5                10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
 15                20                25                30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
    35                40                45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
    50                55                60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
    65                70                75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
    80                85                90

Glu Thr Ala Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp
    95                100                105                110

Phe Ser Pro Ile Asp *
                115

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F02090"95292860

(2) INFORMATION FOR SEQ. ID NO: 11

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 3.4

(ix) FEATURES

- (D) OTHER INFORMATION: Mature Protein for Clone 3.4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

```

Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys
1           5           10           15
Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val Arg Thr
20           25           30
Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu Cys Phe
35           40           45
Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu
50           55           60
Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp
65           70           75           80
Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr
85           90           95
Ala Tyr Asp Thr Phe Lys Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser
100          105          110
Pro Ile Asp *
115

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09876796-060701

(2) INFORMATION FOR SEQ. ID NO: 12

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3.9

(ix) FEATURES

(D) OTHER INFORMATION: Non-His-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

```

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC      46
      Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala
                -15                      -10

ATC GTC ATC GGA GCT CAG GCT CTC ACC GAT GAA CAG ATA CAG AAA      91
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys
      -5                      1                      5

AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GAG TCC GGA GTG TCC     136
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Glu Ser Gly Val Ser
    10                      15                      20

CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT     181
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
    25                      30                      35

CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AGA ACT GGA     226
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Arg Thr Gly
    40                      45                      50

GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC     271
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala
    55                      60                      65

AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG     316
Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val
    70                      75                      80

CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT     361
Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr
    85                      90                      95

GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT     406
Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro
   100                      105                      110

ATT GAT TAA TTGTTTTGTA TTTGACTGAA TTTTGACAAT AAAGGTACTA      455
Ile Asp *
   115

TCGTTATGAA AAAAAAAAAA AAAAAAA      482

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(2) INFORMATION FOR SEQ. ID NO: 13

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 3.9

(ix) FEATURES

- (D) OTHER INFORMATION: Precursor Protein for Clone 3.9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

```

Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala
  -15                      -10                      -5

Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
    1                      5                      10

Glu Cys Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
 15                      20                      25                      30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
    35                      40                      45

Cys Phe Ser Lys Arg Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
    50                      55                      60

Val Glu Val Leu Lys Ala Lys Leu Lys HisVal Ala Ser Asp Glu Glu
    65                      70                      75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
    80                      85                      90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp
 95                      100                      105                      110

Phe Ser Pro Ile Asp *
    115

```

(2) INFORMATION FOR SEQ. ID NO: 14

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 3.9

(ix) FEATURES

- (D) OTHER INFORMATION: Mature protein for Clone 3.9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys
 1 5 10 15
 Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val Arg Thr
 20 25 30
 Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu Cys Phe
 35 40 45
 Ser Lys Arg Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu
 50 55 60
 Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp
 65 70 75 80
 Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr
 85 90 95
 Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser
 100 105 110
 Pro Ile Asp *
 115

09876795-060701

(2) INFORMATION FOR SEQ. ID NO: 15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 7.5

(ix) FEATURES

- (D) OTHER INFORMATION: Non-his-tagged, Signal plus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

```

GGCACGAGCA AAA ATG AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC      46
      Met Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala
                -15                      -10

ATC GTC ATC GGA GCT CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA      90
Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys
      -5                      1                      5

AGG AAC AAG ATC AGC AAA GAG TGC CAG CAG GTG TCC GGA GTG TCC     136
Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val Ser
      10                      15                      20

CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT     181
Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
      25                      30                      35

CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA     226
Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly
      40                      45                      50

GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC     271
Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala
      55                      60                      65

AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG     316
Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val
      70                      75                      80

CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT     361
Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr
      85                      90                      95

GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT     406
Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro
      100                      105                      110

ATT GAT TAA TTGTTTTGTA TTTGGCTGAA TTTTGACAAT AAAGGTACTA      455
Ile Asp *
      115

TCGTTATGTA AAAAAAAAAA AAAAAA      481

```


(2) INFORMATION FOR SEQ. ID NO: 16

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 681 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

```
(iv) ANTI-SENSE: no
```

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
(B) INDIVIDUAL/ISOLATE: none
(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
(B) CLONE: 2.2

(ix) FEATURES

- (D) OTHER INFORMATION: His-tagged, Signal plus

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTA CTTTAAG 50

AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT 141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly
-45 -40 -35

GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG 186
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met
-30 -25 -20

AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC ATC GTC ATC GGA GCT 231
Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala
-15 -10 -5

CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC 276
Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser
1 5 10

AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC 321
Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp
15 20 25

AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT CCC AAA ATG AAG AAG 366
Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys
30 35 40

CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC 411
His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala
45 50 55

GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG 456
Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val
60 65 70

GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC 501
Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val
75 80 85

AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT 546
Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys
90 95 100

ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTGTGTA 595
Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *
105 110 115

TTTGACTGAA TTTTGACAAT AAAGGTAATA TCGTTATGTA AAAAAAAAAA 645

AAAAAACTCG AGCACCACCA CCACCACCAC TGAGAT 681

(2) INFORMATION FOR SEQ. ID NO: 17

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 2.2

(ix) FEATURES

(D) OTHER INFORMATION: Precursor Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

```

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
   -55                               -50                               -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
   -40                               -35                               -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Leu Cys Phe Ala
   -25                               -20                               -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile
  -10                               -5                               1                               5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val
   10                               15                               20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
   25                               30                               35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly Val
   40                               45                               50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu
   55                               60                               65                               70

Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys
   75                               80                               85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys
   90                               95                               100

Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *
  105                               110                               115

```

09876796-050701

(2) INFORMATION FOR SEQ. ID NO: 18

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 543 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.2

(ix) FEATURES

- (D) OTHER INFORMATION: His-tagged, signal minus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-30 -25	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-20 -15 -10	
GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG	186
Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln	
-5 1 5	
AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG	231
Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val	
10 15 20	
TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT	276
Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp	
25 30 35	
GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT	321
Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr	
40 45 50	
GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA	366
Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys	
55 60 65	
GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC	411
Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile	
70 75 80	
GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT	456
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala	
85 90 95	
TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT	501
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser	
100 105 110	
CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT	543
Pro Ile Asp *	
115	

(2) INFORMATION FOR SEQ. ID NO: 19

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 2.2

```
(ix)FEATURES
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(D) OTHER INFORMATION: Mature Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
-30 -25 -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
-15 -10 -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
35 40 45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
80 85 90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp
95 100 105 110

Phe Ser Pro Ile Asp *
115

```

(2) INFORMATION FOR SEQ. ID NO: 20
  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 682 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear
  (ii) MOLECULE TYPE: cDNA to mRNA
  (iii) HYPOTHETICAL: no
  (iv) ANTI-SENSE: no
  (vi) ORIGINAL SOURCE:
      (A) ORGANISM: Tenebrio molitor
      (B) INDIVIDUAL/ISOLATE: none
      (C) CELL TYPE: fat body and whole organism
  (vii) IMMEDIATE SOURCE:
      (A) LIBRARY: cDNA
      (B) CLONE: 2.3
  (ix) FEATURES
      (D) OTHER INFORMATION: His-tagged, Signal Plus

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-55 -50	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-45 -40 -35	
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG	186
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met	
-30 -25 -20	
AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC ATC GTC ATC GGA GCT	231
Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala	
-15 -10 -5	
CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC	276
Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser	
1 5 10	
AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC	321
Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp	
15 20 25	
AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT CCC AAA ATG AAG AAG	366
Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys	
30 35 40	
CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC	411
His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala	
45 50 55	
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG	456
Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val	
60 65 70	
GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC	501
Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val	
75 80 85	
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT	546
Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys	
90 95 100	
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTTGTA	595
Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *	
105 110 115	
TTTGACTGAA TTTTGACAAT AAAGGTACTA TCGTTATGAA AAAAAAAAAA	645
AAAAAAAACTC GAGCACCACC ACCACCACCA CTGAGAT	682

09876756 - 060701
 T02030" 9672860

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: Amino Acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 2.3

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(ix)FEATURES
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(D) OTHER INFORMATION: Precursor Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
-55 -50 -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
-40 -35 -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Leu Cys Phe Ala
-25 -20 -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile
-10 -5 1 5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val
10 15 20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
25 30 35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly Val
40 45 50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu
55 60 65 70

Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys
75 80 85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys
90 95 100

Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *
105 110 115

- (2) INFORMATION FOR SEQ. ID NO: 22
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 543 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.3
 - (ix) FEATURES
 - (D) OTHER INFORMATION: His-tagged, Signal minus
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-30 -25	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-20 -15 -10	
GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG	186
Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln	
-5 1 5	
AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GTG TCC GGA GTG	231
Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val	
10 15 20	
TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAT	276
Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp	
25 30 35	
GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT	321
Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr	
40 45 50	
GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA	366
Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys	
55 60 65	
GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC	411
Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile	
70 75 80	
GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT	456
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala	
85 90 95	
TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT	501
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser	
100 105 110	
CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT	543
Pro Ile Asp *	
115	

(2) INFORMATION FOR SEQ. ID NO: 23

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 2.3

(ix) FEATURES

(D) OTHER INFORMATION: Mature Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
-30 -25 -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
-15 -10 -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
1 5 10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
35 40 45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
80 85 90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp
95 100 105 110

Phe Ser Pro Ile Asp *
115

(2) INFORMATION FOR SEQ. ID NO: 24

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 777 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 13.17

(ix) FEATURES

(D) OTHER INFORMATION: His-tagged, Signal plus

T02090-060701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG 50
 AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC 96
 Met Gly Ser Ser His His His His His Ser
 -65 -60 -55
 AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT 141
 Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly
 -50 -45 -40
 GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC TGG ATC CAA AGA ATT 186
 Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Trp Ile Gln Arg Ile
 -35 -30 -25
 CGG CAC GAG ACT ACT AAG ATG AAG TTG CTC TGT TGT CTA ATC TCC 231
 Arg His Glu Thr Thr Lys Met Lys Leu Leu Cys Cys Leu Ile Ser
 -20 -15 -10
 CTC ATT CTG TTG GTC ACA GTT CAG GCC CTG ACC GAG GCA CAA ATT 276
 Leu Ile Leu Leu Val Thr Val Gln Ala Leu Thr Glu Ala Gln Ile
 -5 1 5
 GAG AAA CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA AGT GGA 321
 Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly
 10 15 20
 GTG TCG CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC TGG GAG 366
 Val Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu
 25 30 35
 GAC GAT CCT AAA CTG AAA CGC CAA GTT TTT TGC GTG GCC AGG AAC 411
 Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn
 40 45 50
 GCC GGT CTG GCC ACG GAA TCG GGA GAG GTG GTG GTC GAC GTG TTG 456
 Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu
 55 60 65
 AGG GAG AAG GTG AGG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAG 501
 Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu
 70 75 80
 AAA ATC ATC AAT AAG TGC GCC GTC AAG AGA GAT ACT GTT GAA GAG 546
 Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu
 85 90 95
 ACG GTG TTC AAT ACT TTC AAA TGT GTC ATG AAA AAC AAG CCA AAG 595
 Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys
 100 105 110
 TTC TCA CCA GTT GAT TGA ACCACCACGA CTAGTAGATG GTTCAAATGG 643
 Phe Ser Pro Val Asp *
 115
 TGTGCTTTAC ATATAAAAT AAAGTGTTTC TGATGTAAAA AAAAAAAAAA 693
 AAAAAAAAAA AACTCGAGAG TATTCTAGAG CGGCCGCGGG CCCATCGTTT 743
 TCCACCCCTC GAGCACCACC ACCACCACCA CTGAGAT 777

(2) INFORMATION FOR SEQ. ID NO: 25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 13.17

(ix) FEATURES

(D) OTHER INFORMATION: Precursor Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

```

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
-55                               -50                               -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
-40                               -35                               -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Cys Cys Leu Ile
-25                               -20                               -15                               -10

Ser Leu Ile Leu Leu Val Thr Val Gln Ala Leu Thr Glu Ala Gln Ile
-5                               1                               5

Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly Val
10                               15                               20

Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu Asp Asp
25                               30                               35

Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn Ala Gly Leu
40                               45                               50

Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu Arg Glu Lys Val
55                               60                               65                               70

Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu Lys Ile Ile Asn Lys
75                               80                               85

Cys Ala Val Lys Arg Asp Thr Val Glu Glu Thr Val Phe Asn Thr Phe
90                               95                               100

Lys Cys Val Met Lys Asn Lys Pro Lys Phe Ser Pro Val Asp *
105                               110                               115

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0587696-060701

- (2) INFORMATION FOR SEQ. ID NO: 26
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 543 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA to mRNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: cDNA
 - (B) CLONE: 13.17
- (ix) FEATURES
- (D) OTHER INFORMATION: His-tagged, Signal minus
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-30 -25	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-20 -15 -10	
GGA CAG CAA ATG GGT CGC GGC CTG ACC GAG GCA CAA ATT GAG AAA	186
Gly Gln Gln Met Gly Arg Gly Leu Thr Glu Ala Gln Ile Glu Lys	
-5 1 5	
CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA AGT GGA GTG TCG	231
Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly Val Ser	
10 15 20	
CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC TGG GAG GAC GAT	276
Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu Asp Asp	
25 30 35	
CCT AAA CTG AAA CGC CAA GTT TTT TGC GTG GCC AGG AAC GCC GGT	321
Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn Ala Gly	
40 45 50	
CTG GCC ACG GAA TCG GGA GAG GTG GTG GTC GAC GTG TTG AGG GAG	366
Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu Arg Glu	
55 60 65	
AAG GTG AGG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAG AAA ATC	411
Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu Lys Ile	
70 75 80	
ATC AAT AAG TGC GCC GTC AAG AGA GAT ACT GTT GAA GAG ACG GTG	456
Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu Thr Val	
85 90 95	
TTC AAT ACT TTC AAA TGT GTC ATG AAA AAC AAG CCA AAG TTC TCA	501
Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys Phe Ser	
100 105 110	
CCA GTT GAT TGA CTCGAGCACC ACCACCACCA CCACTGAGAT	543
Pro Val Asp *	
115	

(2) INFORMATION FOR SEQ. ID NO: 27

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 13.17

(ix) FEATURES

- (D) OTHER INFORMATION: Mature Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

```

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
   -30                               -25                               -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
   -15                               -10                               -5

Gly Leu Thr Glu Ala Gln Ile Glu Lys Leu Asn Lys Ile Ser Lys Lys
   1                               5                               10                               15

Cys Gln Asn Glu Ser Gly Val Ser Gln Glu Ile Ile Thr Lys Ala Arg
   20                               25                               30

Asn Gly Asp Trp Glu Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys
   35                               40                               45

Val Ala Arg Asn Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val
   50                               55                               60

Asp Val Leu Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu
   65                               70                               75

Thr Glu Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu
   80                               85                               90                               95

Glu Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys
   100                              105                              110

Phe Ser Pro Val Asp *
   115

```

- (2) INFORMATION FOR SEQ. ID NO: 28
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 681 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 3.4
 - (ix) FEATURES
 - (D) OTHER INFORMATION: His-tagged, Signal plus

060701-060701

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

	TTGTTAGCGG	ATGGAATTCC	CTCGTAGGGG	ATAATTTTGT	TTACTTTAAG		50
AAGGAGATAT	ACC	ATG GGC AGC	AGC CAT CAT CAT CAT CAC AGC				96
		Met Gly Ser	Ser His His His His His Ser	-55	-50		
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT							141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly							
		-45					
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG							186
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met							
		-30					
AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC ATC GTC ATC GGA GCT							231
Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala							
		-15					
CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC							276
Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser							
		1					
AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC							321
Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp							
		15					
AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT CCC AAA ATG AAG AAG							366
Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys							
		30					
CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC							411
His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala							
		45					
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG							456
Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val							
		60					
GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC							501
Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val							
		75					
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG GTT							546
Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Val							
		90					
ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTTGTA							595
Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *							
		105					
TTTGACTGAA TTTTGACAAT AAAGGTACTA TC GTTATGTA AAAAAAAAAA							645
AAAAAAAACTCG AGCACCAACCA CCACCAACCAC TGAGAT							681

(2) INFORMATION FOR SEQ. ID NO: 29

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3.4

(ix) FEATURES

(D) OTHER INFORMATION: Precursor protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
-55 -50 -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
-40 -35 -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Leu Cys Phe Ala
-25 -20 -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile
-10 -5 1 5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val
10 15 20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
25 30 35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly Val
40 45 50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu
55 60 65 70

Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys
75 80 85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys
90 95 100

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Val Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *
      105                      110                      115
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3

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100

11

1000

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- RB125 SEQ

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG

AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC
Met Gly Ser Ser His His His His His His Ser
-55 -50

96

AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly
-45 -40 -35

141

GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG
Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met
-30 -25 -20

186

AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC ATC GTC ATC GGA GCT
Lys Leu Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala
-15 -10 -5

231

CAG GCT CTC ACC GAT GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC
Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser

276

AAA GAA TGC CAG CAG GAG TCC GGA GTG TCC CAA GAG ACG ATC GAC
Lys Glu Cys Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp
15 20 25

321

AAA GTC CGC ACA GGT GTC TTG GTC GAC GAT CCC AAA ATG AAG AAG
Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys
30 35 40

366

CAC GTC CTC TGC TTC TCG AAG AGA ACT GGA GTG GCA ACC GAA GCC
His Val Leu Cys Phe Ser Lys Arg Thr Gly Val Ala Thr Glu Ala
45 50 55

411

GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG
Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val

456

GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC
Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val
75 80 85

501

AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT
Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys

546

ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTTGTA
Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *
105 110 115

595

TTTGACTGAA TTTTGACAAT AAAGGTACTA TCGTTATGAA AAAAAAAAAA

645

AAAAAAAACTC GAGCACCACC ACCACCACCA CTGAGAT

682

(2) INFORMATION FOR SEQ. ID NO: 33

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3.9

(ix) FEATURES

(D) OTHER INFORMATION: Precursor Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
-55 -50 -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
-40 -35 -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Leu Cys Phe Ala
-25 -20 -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile
-10 -5 1 5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Glu Ser Gly Val
10 15 20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
25 30 35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Arg Thr Gly Val
40 45 50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu
55 60 65 70

Lys HisVal Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys
75 80 85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys
90 95 100

Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *
105 110 115

- (2) INFORMATION FOR SEQ. ID NO: 34
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 543 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 3.9
 - (ix) FEATURES
 - (D) OTHER INFORMATION: His-tagged, Signal minus
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-30 -25	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-20 -15 -10	
GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAT GAA CAG ATA CAG	186
Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln	
-5 1 5	
AAA AGG AAC AAG ATC AGC AAA GAA TGC CAG CAG GAG TCC GGA GTG	231
Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Glu Ser Gly Val	
10 15 20	
TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC	276
Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp	
25 30 35	
GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AGA ACT	321
Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Arg Thr	
40 45 50	
GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA	366
Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys	
55 60 65	
GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAA GTG GAC AAG ATC	411
Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile	
70 75 80	
GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT	456
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala	
85 90 95	
TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT	501
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser	
100 105 110	
CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT	543
Pro Ile Asp *	
115	

(2) INFORMATION FOR SEQ. ID NO: 35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 3.9

(ix) FEATURES

(D) OTHER INFORMATION: Mature Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
-30 -25 -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
-15 -10 -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys

Glu Cys Gln Gln Glu Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
35 40 45

Cys Phe Ser Lys Arg Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys HisVal Ala Ser Asp Glu Glu
65 70 75Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
80 85 90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp
95 100 105 110

Phe Ser Pro Ile Asp *
115

- (2) INFORMATION FOR SEQ. ID NO: 36
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 681 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 7.5
 - (ix) FEATURES
 - (D) OTHER INFORMATION: His-tagged, Signal plus

096796-060201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

TTGTTAGCGG	ATGGAATTCC	CTCGTAGGGG	ATAATTTTGT	TTACTTTAAG	50										
AAGGAGATAT	ACC	ATG	GGC	AGC	AGC	CAT	CAT	CAT	CAT	CAT	CAC	AGC	96		
		Met	Gly	Ser	Ser	His	His	His	His	His	His	Ser			
				-55								-50			
AGC	GGC	CTG	GTG	CCG	CGC	GGC	AGC	CAT	ATG	GCT	AGC	ATG	ACT	GGT	141
Ser	Gly	Leu	Val	Pro	Arg	Gly	Ser	His	Met	Ala	Ser	Met	Thr	Gly	
	-45					-40					-35				
GGA	CAG	CAA	ATG	GGT	CGC	GGA	TCC	GAA	TTC	GCA	CGA	GCA	AAA	ATG	186
Gly	Gln	Gln	Met	Gly	Arg	Gly	Ser	Glu	Phe	Ala	Arg	Ala	Lys	Met	
	-30					-25					-20				
AAA	CTC	CTC	TTG	TGC	TTT	GCG	TTC	GCC	GCC	ATC	GTC	ATC	GGA	GCT	231
Lys	Leu	Leu	Leu	Cys	Phe	Ala	Phe	Ala	Ala	Ile	Val	Ile	Gly	Ala	
	-15					-10					-5				
CAG	GCT	CTC	ACC	GAC	GAA	CAG	ATA	CAG	AAA	AGG	AAC	AAG	ATC	AGC	276
Gln	Ala	Leu	Thr	Asp	Glu	Gln	Ile	Gln	Lys	Arg	Asn	Lys	Ile	Ser	
	1				5						10				
AAA	GAG	TGC	CAG	CAG	GTG	TCC	GGA	GTG	TCC	CAA	GAG	ACG	ATC	GAC	321
Lys	Glu	Cys	Gln	Gln	Val	Ser	Gly	Val	Ser	Gln	Glu	Thr	Ile	Asp	
	15					20					25				
AAA	GTC	CGC	ACA	GGT	GTC	TTG	GTC	GAC	GAT	CCC	AAA	ATG	AAG	AAG	366
Lys	Val	Arg	Thr	Gly	Val	Leu	Val	Asp	Asp	Pro	Lys	Met	Lys	Lys	
	30					35					40				
CAC	GTC	CTC	TGC	TTC	TCG	AAG	AAA	ACT	GGA	GTG	GCA	ACC	GAA	GCC	411
His	Val	Leu	Cys	Phe	Ser	Lys	Lys	Thr	Gly	Val	Ala	Thr	Glu	Ala	
	45					50					55				
GGA	GAC	ACC	AAT	GTG	GAG	GTA	CTC	AAA	GCC	AAG	CTG	AAG	CAT	GTG	456
Gly	Asp	Thr	Asn	Val	Glu	Val	Leu	Lys	Ala	Lys	Leu	Lys	His	Val	
	60					65					70				
GCC	AGC	GAC	GAA	GAG	GTG	GAC	AAG	ATC	GTG	CAG	AAG	TGC	GTG	GTC	501
Ala	Ser	Asp	Glu	Glu	Val	Asp	Lys	Ile	Val	Gln	Lys	Cys	Val	Val	
	75					80					85				
AAG	AAG	GCC	ACA	CCA	GAG	GAA	ACG	GCT	TAT	GAC	ACC	TTC	AAG	TGT	546
Lys	Lys	Ala	Thr	Pro	Glu	Glu	Thr	Ala	Tyr	Asp	Thr	Phe	Lys	Cys	
	90					95					100				
ATT	TAC	GAC	AGT	AAA	CCT	GAT	TTC	TCT	CCT	ATT	GAT	TAA	TTGTTTTGTA	595	
Ile	Tyr	Asp	Ser	Lys	Pro	Asp	Phe	Ser	Pro	Ile	Asp	*			
	105					110					115				
TTTGGCTGAA	TTTTGACAAT	AAAGGTACTA	TCGTTATGTA	AAAAAAAAAA	645										
AAAAAACTCG	AGCACCACCA	CCACCACCAC	TGAGAT	681											

(2) INFORMATION FOR SEQ. ID NO: 37

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 7.5

(ix) FEATURES

(D) OTHER INFORMATION: Precursor Protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37

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Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
   -55                               -50                               -45

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
   -40                               -35                               -30

Gly Ser Glu Phe Ala Arg Ala Lys Met Lys Leu Leu Leu Cys Phe Ala
   -25                               -20                               -15

Phe Ala Ala Ile Val Ile Gly Ala Gln Ala Leu Thr Asp Glu Gln Ile
  -10                               -5                               1                               5

Gln Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val
   10                               15                               20

Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp Asp
   25                               30                               35

Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr Gly Val
   40                               45                               50

Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu
   55                               60                               65                               70

Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys
   75                               80                               85

Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys
   90                               95                               100

Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp *
  105                               110                               115

```

(2) INFORMATION FOR SEQ. ID NO: 38

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 543 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 7.5

(ix) FEATURES

(D) OTHER INFORMATION: His-tagged, Signal minus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC	96
Met Gly Ser Ser His His His His His His Ser	
-30 -25	
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT	141
Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly	
-20 -15 -10	
GGA CAG CAA ATG GGT CGC GGA TCC CTC ACC GAC GAA CAG ATA CAG	186
Gly Gln Gln Met Gly Arg Gly Ser Leu Thr Asp Glu Gln Ile Gln	
-5 1 5	
AAA AGG AAC AAG ATC AGC AAA GAG TGC CAG CAG GTG TCC GGA GTG	231
Lys Arg Asn Lys Ile Ser Lys Glu Cys Gln Gln Val Ser Gly Val	
10 15 20	
TCC CAA GAG ACG ATC GAC AAA GTC CGC ACA GGT GTC TTG GTC GAC	276
Ser Gln Glu Thr Ile Asp Lys Val Arg Thr Gly Val Leu Val Asp	
25 30 35	
GAT CCC AAA ATG AAG AAG CAC GTC CTC TGC TTC TCG AAG AAA ACT	321
Asp Pro Lys Met Lys Lys His Val Leu Cys Phe Ser Lys Lys Thr	
40 45 50	
GGA GTG GCA ACC GAA GCC GGA GAC ACC AAT GTG GAG GTA CTC AAA	366
Gly Val Ala Thr Glu Ala Gly Asp Thr Asn Val Glu Val Leu Lys	
55 60 65	
GCC AAG CTG AAG CAT GTG GCC AGC GAC GAA GAG GTG GAC AAG ATC	411
Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu Val Asp Lys Ile	
70 75 80	
GTG CAG AAG TGC GTG GTC AAG AAG GCC ACA CCA GAG GAA ACG GCT	456
Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu Glu Thr Ala	
85 90 95	
TAT GAC ACC TTC AAG TGT ATT TAC GAC AGT AAA CCT GAT TTC TCT	501
Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp Phe Ser	
100 105 110	
CCT ATT GAT TAA CTCGAGCACC ACCACCACCA CCACTGAGAT	543
Pro Ile Asp *	
115	

(2) INFORMATION FOR SEQ. ID NO: 39

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 Amino Acids

(B) TYPE: Amino Acid

(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear
```

(ii) MOLECULE TYPE: Protein

(iii) HYPOTHETICAL: no

```
(iv) ANTI-SENSE: no
```

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 7.5

(ix) FEATURES

(D) OTHER INFORMATION: Mature protein with His-tag

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
-30 -25 -20

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg
-15 -10 -5

Gly Ser Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser Lys
1 5 10

Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp Lys Val
15 20 25 30

Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys His Val Leu
35 40 45

Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala Gly Asp Thr Asn
50 55 60

Val Glu Val Leu Lys Ala Lys Leu Lys His Val Ala Ser Asp Glu Glu
65 70 75

Val Asp Lys Ile Val Gln Lys Cys Val Val Lys Lys Ala Thr Pro Glu
80 85 90

Glu Thr Ala Tyr Asp Thr Phe Lys Cys Ile Tyr Asp Ser Lys Pro Asp
95 100 105 110

Phe Ser Pro Ile Asp *
115

- (2) INFORMATION FOR SEQ. ID NO: 40
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.2, 2.3, 3.4, 3.9, and 7.5
 - (ix) FEATURES
 - (D) OTHER INFORMATION: Tm 12.84 upper primer with Bam-HI site
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

CGCGGATCCC TCACCGACGA ACAG 24

104090-962350

- (2) INFORMATION FOR SEQ. ID NO: 41
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (iii) HYPOTHETICAL: no
 - (iv) ANTI-SENSE: no
 - (v) ORIGINAL SOURCE:
 - (A) ORGANISM: *Tenebrio molitor*
 - (B) INDIVIDUAL/ISOLATE: none
 - (C) CELL TYPE: fat body and whole organism
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: cDNA
 - (B) CLONE: 2.2, 2.3, 3.4, 3.9, and 7.5
 - (ix) FEATURES
 - (D) OTHER INFORMATION: Tm 12.84 lower primer with XhoI site
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

GAGAGGATAA CTAATTGAGC TCGCC 25

092696-060701

(2) INFORMATION FOR SEQ. ID NO: 42

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 13.17

(ix) FEATURES

(D) OTHER INFORMATION: Tm 13.17 upper primer with Bam-H1 site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

CGCGGATCCC TGACCGAGGC ACAA 24

T02090" 96292860

(2) INFORMATION FOR SEQ. ID NO: 43

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 13.17

(ix) FEATURES

(D) OTHER INFORMATION: Tm 13.17 lower primer with XhoI site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

GAGTGGTCAA CTAACGAGC TCGCC 25

T02030" 95292860

(2) INFORMATION FOR SEQ. ID NO: 44

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(v)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE: 2.2

(ix) FEATURES

- (D) OTHER INFORMATION: Consensus of the Tm 12.84 Isoforms

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

GGCACGAGCA	AAA	ATG	AAA	CTC	CTC	TTG	TGC	TTT	GCN	TTC	GCC	GCC		46
		Met	Lys	Leu	Leu	Leu	Cys	Phe	Ala	Phe	Ala	Ala		
				-15								-10		
ATC	GTC	ATC	GGA	GCT	CAG	GCT	CTC	ACC	GAY	GAA	CAG	ATA	CAG	AAA
Ile	Val	Ile	Gly	Ala	Gln	Ala	Leu	Thr	Asp	Glu	Gln	Ile	Gln	Lys
		-5				1				5				91
AGG	AAC	AAG	ATC	AGC	AAA	GAR	TGC	CAG	CAG	GNG	TCC	GGA	GTG	TCC
Arg	Asn	Lys	Ile	Ser	Lys	Glu	Cys	Gln	Gln	Val	Ser	Gly	Val	Ser
	10					15					20			136
CAA	GAG	ACG	ATC	GAC	AAA	GTC	CGC	ACA	GGT	GTC	TTG	GTC	GAY	GAT
Gln	Glu	Thr	Ile	Asp	Lys	Val	Arg	Thr	Gly	Val	Leu	Val	Asp	Asp
	25					30					35			181
CCC	AAA	ATG	AAG	AAG	CAC	GTC	CTC	TGC	TTC	TCG	AAG	ARA	ACT	GGA
Pro	Lys	Met	Lys	Lys	His	Val	Leu	Cys	Phe	Ser	Lys	Lys	Thr	Gly
	40					45					50			226
GTG	GCA	ACC	GAA	GCC	GGA	GAC	ACC	AAT	GTG	GAG	GTA	CTC	AAA	GCC
Val	Ala	Thr	Glu	Ala	Gly	Asp	Thr	Asn	Val	Glu	Val	Leu	Lys	Ala
	55					60					65			271
AAG	CTG	AAG	CAT	GTG	GCC	AGC	GAC	GAA	GAR	GTG	GAC	AAG	ATC	GTG
Lys	Leu	Lys	His	Val	Ala	Ser	Asp	Glu	Glu	Val	Asp	Lys	Ile	Val
	70					75					80			316
CAG	AAG	TGC	GTG	GTC	AAG	AAG	GCC	ACA	CCA	GAG	GAA	ACG	GCT	TAT
Gln	Lys	Cys	Val	Val	Lys	Lys	Ala	Thr	Pro	Glu	Glu	Thr	Ala	Tyr
	85					90					95			361
GAC	ACC	TTC	AAG	NNT	ATT	TAC	GAC	AGT	AAA	CCT	GAT	TTC	TCT	CCT
Asp	Thr	Phe	Lys	Cys	Ile	Tyr	Asp	Ser	Lys	Pro	Asp	Phe	Ser	Pro
	100					105					110			406
ATT	GAT	TAA	TTGTTTGTGTA	TTTGRCTGAA	TTTTGACAAT	AAAGGTANTA								
Ile	Asp	*												455
	115													
TCGTTATGNA	AAAAAAAAAAAA	AAAAAA												481

(2) INFORMATION FOR SEQ. ID NO: 45

- ```

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 481 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA to mRNA
(iii) HYPOTHETICAL: no
(iv) ANTI-SENSE: no
(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Tenebrio molitor
 (B) INDIVIDUAL/ISOLATE: none
 (C) CELL TYPE: fat body and whole organism
(vii) IMMEDIATE SOURCE:
 (A) LIBRARY: cDNA
 (B) CLONE: 2.2
(ix) FEATURES
 (D) OTHER INFORMATION: Consensus of Seq ID #44 with Tm 13.17
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

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[illegible]

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(2) INFORMATION FOR SEQ. ID NO: 46
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 481 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA to mRNA
 (iii) HYPOTHETICAL: no
 (iv) ANTI-SENSE: no
 (v)
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Tenebrio molitor
 (B) INDIVIDUAL/ISOLATE: none
 (C) CELL TYPE: fat body and whole organism
 (vii) IMMEDIATE SOURCE:
 (A) LIBRARY: cDNA
 (B) CLONE: 2.2
 (ix) FEATURES
 (D) OTHER INFORMATION: Consensus of Seq ID #45 with B1/B2
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

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[illegible]

## (2) INFORMATION FOR SEQ. ID NO: 47

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 481 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Tenebrio molitor*

(B) INDIVIDUAL/ISOLATE: none

(C) CELL TYPE: fat body and whole organism

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: cDNA

(B) CLONE: 2.2

(ix) FEATURES

(D) OTHER INFORMATION: Consensus of Seq. ID #46 with AFP-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

|            |            |        |     |            |             |            |            |     |     |     |     |     |     |     |     |
|------------|------------|--------|-----|------------|-------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|
| GGC        | NNR        | NNNN   | AAR | ATG        | AAR         | YTN        | CTC        | YNN | TGY | YTN | RYN | YYY | NYN | RYY | 46  |
|            |            |        | Met | Lys        | Leu         | Leu        | Leu        | Cys | Phe | Ala | Phe | Ala | Ala |     |     |
|            |            |        |     |            |             |            | -15        |     |     |     |     |     | -10 |     |     |
|            |            |        |     |            |             |            |            |     |     |     |     |     |     |     |     |
| NTN        | NTN        | RYC    | NNR | RYY        | YAN         | GCT        | NTN        | ACY | NAN | RNA | NNN | NNN | NAG | NNR | 91  |
| Ile        | Val        | Ile    | Gly | Ala        | Gln         | Ala        | Leu        | Thr | Asp | Glu | Gln | Ile | Gln | Lys |     |
|            |            | -5     |     |            |             |            | 1          |     |     |     | 5   |     |     |     |     |
|            |            |        |     |            |             |            |            |     |     |     |     |     |     |     |     |
| NNG        | NNY        | NAR    | NNC | AGC        | RNN         | RNN        | TGY        | NAR | NNN | GNR | NNY | GGA | GTR | TCN | 136 |
| Arg        | Asn        | Lys    | Ile | Ser        | Lys         | Glu        | Cys        | Gln | Gln | Glu | Ser | Gly | Val | Ser |     |
|            | 10         |        |     |            |             | 15         |            |     |     |     | 20  |     |     |     |     |
|            |            |        |     |            |             |            |            |     |     |     |     |     |     |     |     |
| NAA        | GAN        | NYN    | NTN | RNN        | ARR         | GYY        | CGC        | ANN | NGT | GNN | NNR | GNN | GAY | GAY | 181 |
| Gln        | Glu        | Thr    | Ile | Asp        | Lys         | Val        | Arg        | Thr | Gly | Val | Leu | Val | Asp | Asp |     |
|            | 25         |        |     |            |             | 30         |            |     |     |     | 35  |     |     |     |     |
|            |            |        |     |            |             |            |            |     |     |     |     |     |     |     |     |
| CCY        | AAA        | NTG    | AAR | NNN        | CAN         | YYY        | YTY        | TGC | NTN | NYN | ARG | RNN | YYY | GRN | 226 |
| Pro        | Lys        | Met    | Lys | Lys        | His         | Val        | Leu        | Cys | Phe | Ser | Lys | Lys | Thr | Gly |     |
|            | 40         |        |     |            |             | 45         |            |     |     |     | 50  |     |     |     |     |
|            |            |        |     |            |             |            |            |     |     |     |     |     |     |     |     |
| NTN        | RYN        | RNN    | GNN | NNN        | GGN         | GAN        | NYN        | NNN | NYN | GAN | NNN | NTN | ARR | RNN | 271 |
| Val        | Ala        | Thr    | Glu | Ala        | Gly         | Asp        | Thr        | Asn | Val | Glu | Val | Leu | Lys | Ala |     |
|            | 55         |        |     |            |             | 60         |            |     |     |     | 65  |     |     |     |     |
|            |            |        |     |            |             |            |            |     |     |     |     |     |     |     |     |
| AAR        | NTN        | ANG    | NRN | NNN        | NNN         | RNN        | RNN        | NNN | RAR | RAR | RYN | RRN | RRN | NTN | 316 |
| Lys        | Leu        | Lys    | His | Val        | Ala         | Ser        | Asn        | Asp | Glu | Glu | Val | Asp | Lys | Ile |     |
|            | 70         |        |     |            |             | 75         |            |     |     |     | 80  |     |     |     |     |
|            |            |        |     |            |             |            |            |     |     |     |     |     |     |     |     |
| NYN        | NNN        | ARN    | NNN | NNN        | NNN         | NNG        | ARN        | RNN | NYN | NNN | NAR | NNN | NNN | NNN | 361 |
| Val        | Gln        | Lys    | Cys | Val        | Val         | Lys        | Lys        | Ala | Thr | Pro | Glu | Glu | Thr | Ala |     |
|            | 85         |        |     |            |             | 90         |            |     |     |     | 95  |     |     |     |     |
|            |            |        |     |            |             |            |            |     |     |     |     |     |     |     |     |
| NNN        | RAN        | NYN    | YYN | AAN        | NNN         | NNY        | NNN        | RRN | ANN | ARN | YCN | NNN | TNN | NNN | 406 |
| Tyr        | Asp        | Thr    | Phe | Lys        | Cys         | Ile        | Tyr        | Asp | Ser | Lys | Pro | Asp | Phe | Ser |     |
|            | 100        |        |     |            |             | 105        |            |     |     |     | 110 |     |     |     |     |
|            |            |        |     |            |             |            |            |     |     |     |     |     |     |     |     |
| CNN        | NYN        | RNN    | TRN | NNNNNNNNNN | YNNRRNNNNNN | NNNNNNNAAT | AAANNNNNNN |     |     |     |     |     |     |     | 458 |
| Pro        | Ile        | Asp    | *   |            |             |            |            |     |     |     |     |     |     |     |     |
|            | 115        |        |     |            |             |            |            |     |     |     |     |     |     |     |     |
|            |            |        |     |            |             |            |            |     |     |     |     |     |     |     |     |
| NNNNNNNNNA | AAAAAAAAAA | AAAAAA |     |            |             |            |            |     |     |     |     |     |     |     | 484 |

## (2) INFORMATION FOR SEQ. ID NO: 48

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 Amino Acids
- (B) TYPE: Amino Acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: Protein

## (iii) HYPOTHETICAL: no

## (iv) ANTI-SENSE: no

## (vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Tenebrio molitor*
- (B) INDIVIDUAL/ISOLATE: none
- (C) CELL TYPE: fat body and whole organism

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA
- (B) CLONE:

## (ix) FEATURES

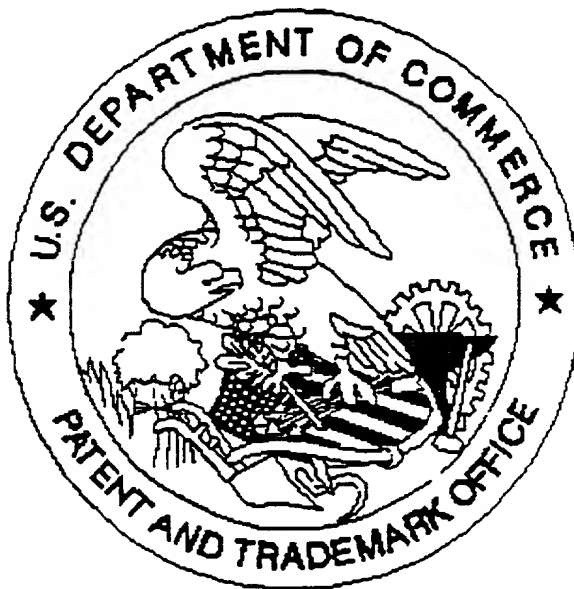
- (D) OTHER INFORMATION: Genral Consensus of Clones,  
B1, B2 and AFP-3

0967696-060704

|                   |                   |                          |                          |                          |                   |                                |                                 |                   |                          |                   |                          |                                |                          |                          |                          |    |  |  |
|-------------------|-------------------|--------------------------|--------------------------|--------------------------|-------------------|--------------------------------|---------------------------------|-------------------|--------------------------|-------------------|--------------------------|--------------------------------|--------------------------|--------------------------|--------------------------|----|--|--|
| Met               | Lys               | Leu                      | Leu                      | Leu<br>Cys               | Cys               | Phe<br>Leu                     | Ala<br>Ile<br>Thr<br>Val        | Phe<br>Ser<br>Leu | Ala<br>Leu<br>Val        | Ala<br>Ile<br>Leu | Ile<br>Val<br>Leu        | Gly<br>Val<br>Ala              | Ala<br>Thr<br>Ala        |                          |                          |    |  |  |
|                   |                   |                          |                          |                          |                   |                                |                                 |                   |                          |                   |                          |                                |                          | Ala<br>Val<br>Thr        |                          |    |  |  |
|                   |                   |                          |                          | -15                      |                   |                                |                                 |                   | -10                      |                   |                          |                                |                          |                          |                          |    |  |  |
| Gln<br>Tyr        | Ala               | Leu<br>Ile               | Thr                      | Asp<br>Glu               | Glu<br>Ala<br>Thr | Gln<br>Asp<br>Pro              | Ile<br>Leu<br>Arg<br>5          | Gln<br>Glu        | Lys<br>Leu               | Arg<br>Leu        | Asn<br>Arg<br>Lys        | Lys<br>Gln<br>10               | Ile<br>Thr<br>His        | Ser                      | Lys<br>Ala<br>Asp        |    |  |  |
|                   |                   | 1                        |                          |                          |                   |                                | 5                               |                   |                          |                   |                          |                                |                          |                          | 10                       |    |  |  |
| Glu<br>Lys<br>Ala | Cys               | Gln<br>Lys               | Gln<br>Asn<br>Thr<br>Ala | Glu<br>Val               | Ser               | Gly                            | Val<br>Ala                      | Ser               | Gln<br>Glu               | Glu<br>Asp<br>Ala | Thr<br>Ile<br>Val<br>Ser | Ile<br>Leu                     | Asp<br>Thr<br>Lys<br>Asn | Lys<br>Arg               | Val<br>Ala               |    |  |  |
|                   |                   | 15                       |                          |                          |                   |                                | 20                              |                   |                          |                   |                          |                                |                          |                          | 25                       |    |  |  |
| Arg               | Thr<br>Asn<br>Lys | Gly<br>Arg               | Val<br>Asp<br>Glu        | Leu<br>Trp<br>Glu        | Val<br>Glu        | Asp                            | Asp                             | Pro               | Lys                      | Met<br>Leu        | Lys                      | Lys<br>Arg<br>Met<br>Glu       | His<br>Gln               | Val<br>Leu<br>Ala        | Leu<br>Phe               |    |  |  |
|                   |                   |                          |                          | 35                       |                   |                                |                                 |                   | 40                       |                   |                          |                                |                          |                          |                          | 45 |  |  |
| Cys               | Phe<br>Val<br>Ile | Ser<br>Ala<br>Phe<br>Leu | Lys<br>Arg               | Lys<br>Arg<br>Ala<br>Asn | Thr<br>Ala<br>Leu | Gly<br>Ile<br>Glu              | Val<br>Leu<br>Ile<br>Glu<br>Phe | Ala<br>Val<br>Ile | Thr<br>Ala<br>Asp        | Glu<br>Ala        | Ala<br>Ser               | Gly                            | Asp<br>Glu               | Thr<br>Ile<br>Val<br>Phe | Asn<br>Glu<br>Val<br>Gln |    |  |  |
|                   |                   |                          |                          | 50                       |                   |                                |                                 |                   | 55                       |                   |                          |                                |                          |                          |                          | 60 |  |  |
| Val<br>Ala<br>Leu | Glu<br>Asp        | Val<br>Thr<br>His        | Leu<br>Phe<br>Ile        | Lys<br>Arg               | Ala<br>Glu<br>Thr | Lys                            | Leu<br>Val<br>Phe               | Lys<br>Thr<br>Arg | His<br>Arg<br>Lys<br>Glu | Val<br>Asn        | Ala<br>Thr<br>Ser        | Ser<br>Asn<br>Asp<br>Glu<br>75 | AAA<br>Asp<br>Asn<br>His | Asp<br>Pro               | Glu                      |    |  |  |
|                   |                   | 65                       |                          |                          |                   |                                | 70                              |                   |                          |                   |                          |                                |                          | 75                       |                          |    |  |  |
| Glu<br>Lys        | Val<br>Ser<br>Thr | Asp<br>Glu               | Lys<br>Asp               | Ile<br>Leu               | Val<br>Ile        | Gln<br>Glu<br>Asn<br>Ala<br>85 | Lys                             | Cys               | Val<br>Ala<br>Thr        | Val               | Val                      | Lys<br>Thr                     | Lys<br>Glu<br>Arg        | Ala<br>Asp               | Thr<br>Val               |    |  |  |
|                   |                   | 80                       |                          |                          |                   |                                | 85                              |                   |                          |                   |                          |                                |                          | 90                       |                          |    |  |  |
| Glu<br>Gln        | Glu<br>Asp<br>His | Thr<br>Ser               | Ala<br>Val<br>Ser        | Tyr<br>Phe<br>Ala        | Asp<br>Glu<br>Asn | Thr<br>Val<br>Phe              | Phe<br>Thr                      | Lys               | Cys<br>Val               | Ile<br>Val        | Tyr<br>Leu<br>Met<br>His | Asp<br>Lys                     | Ser<br>Asn<br>Asp        | Lys<br>Arg               | Pro<br>Ser               |    |  |  |
|                   |                   | 95                       |                          |                          |                   |                                | 100                             |                   |                          |                   |                          |                                |                          | 105                      |                          |    |  |  |
| Asp<br>Asn<br>Lys | Phe               | Ser<br>Phe               | Pro<br>Gly               | Ile<br>Asp<br>Val<br>115 | Asp<br>Leu        | ***<br>Phe                     | ***<br>Val                      | *                 |                          |                   |                          |                                |                          |                          |                          |    |  |  |
|                   |                   |                          |                          | 115                      |                   |                                |                                 |                   |                          |                   |                          |                                |                          |                          |                          |    |  |  |



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*Drawings*

104090-96292860